

0590
0411

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#2

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/024,955

DATE: 04/16/2002
TIME: 16:20:42

Input Set : N:\CrF3\RULE60\10024955.raw
Output Set: N:\CRF3\04162002\J024955.raw

SEQUENCE LISTING

ENTERED

RAW SEQUENCE LISTING

DATE: 04/16/2002

PATENT APPLICATION: US/10/024,955

TIME: 16:20:42

Input Set : N:\Crf3\RULE60\10024955.raw
 Output Set: N:\CRF3\04162002\J024955.raw

62	(B) LOCATION: 68..712																
64	(ix) FEATURE:																
65	(A) NAME/KEY: mat_peptide																
66	(B) LOCATION: 119..712																
69	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:																
71	TTTTTTTTT	TTTGTTAT	TCCCATTTC	TTCATATCGT	AAAAATCCAA	ATTCAC	TTTT	60									
73	TTACCAA	ATG	ATG	AAA	TTA	TTA	TTG	ATT	GCT	GCC	GCA	GCT	TTT	GTT	GCC	109	
74	Met	Met	Lys	Leu	Leu	Ile	Ala	Ala	Ala	Ala	Phe	Val	Ala				
75	-17	-15				-10					-5						
77	GTT	TCG	GCT	GAT	CCA	ATT	CAC	TAT	GAT	AAA	ATC	ACC	GAA	GAA	ATT	AAC	157
78	Val	Ser	Ala	Asp	Pro	Ile	His	Tyr	Asp	Lys	Ile	Thr	Glu	Glu	Ile	Asn	
79	1					5					10						
81	AAA	GCT	GTT	GAT	GAA	GCC	GTC	GCT	GCA	ATT	GAA	AAA	TCC	GAA	ACA	TTC	205
82	Lys	Ala	Val	Asp	Glu	Ala	Val	Ala	Ala	Ile	Glu	Lys	Ser	Glu	Thr	Phe	
83	15					20					25						
85	GAT	CCA	ATG	AAG	GTA	CCC	GAT	CAT	TCT	GAT	AAA	TTC	GAA	CGA	CAT	ATT	253
86	Asp	Pro	Met	Lys	Val	Pro	Asp	His	Ser	Asp	Lys	Phe	Glu	Arg	His	Ile	
87	30					35					40			45			
89	GGT	ATC	ATC	GAT	TTA	AAA	GGT	GAA	TTA	GAC	ATG	CGA	AAC	ATT	CAA	GTT	301
90	Gly	Ile	Ile	Asp	Leu	Lys	Gly	Glu	Leu	Asp	Met	Arg	Asn	Ile	Gln	Val	
91						50					55			60			
93	CGA	GGA	TTA	AAA	CAA	ATG	AAA	CGT	GTA	GGT	GAT	GCT	AAT	GTG	AAA	AGT	349
94	Arg	Gly	Leu	Lys	Gln	Met	Lys	Arg	Val	Gly	Asp	Ala	Asn	Val	Lys	Ser	
95						65					70			75			
97	GAA	GAT	GGT	GTC	AAA	GCT	CAT	TTG	TTG	GTC	GGT	GTT	CAT	GAT	GAC		397
98	Glu	Asp	Gly	Val	Val	Lys	Ala	His	Leu	Leu	Val	Gly	Val	His	Asp	Asp	
99						80					85			90			
101	GTT	GTT	TCA	ATG	GAA	TAT	GAT	TTA	GCA	TAC	AAA	TTG	GGT	GAT	CTT	CAT	445
102	Val	Val	Ser	Met	Glu	Tyr	Asp	Leu	Ala	Tyr	Lys	Leu	Gly	Asp	Leu	His	
103						95					100			105			
105	CCA	AAC	ACT	CAT	GTC	ATT	TCG	GAT	ATT	CAG	GAT	TTT	GTT	GTC	GAA	TTA	493
106	Pro	Asn	Thr	His	Val	Ile	Ser	Asp	Ile	Gln	Asp	Phe	Val	Val	Glu	Leu	
107	110					115					120			125			
109	TCG	CTC	GAA	GTT	AGC	GAA	GAA	GGT	AAT	ATG	ACA	TTG	ACA	TCG	TTC	GAA	541
110	Ser	Leu	Glu	Val	Ser	Glu	Glu	Gly	Asn	Met	Thr	Leu	Thr	Ser	Phe	Glu	
111						130					135			140			
113	GTA	CGT	CAA	TTT	GCC	AAT	GTT	GTC	AAT	CAT	ATT	GGT	GGT	CTT	TCA	ATT	589
114	Val	Arg	Gln	Phe	Ala	Asn	Val	Val	Asn	His	Ile	Gly	Gly	Leu	Ser	Ile	
115						145					150			155			
117	TTG	GAT	CCA	ATT	TTC	GCT	GTC	TTA	TCC	GAT	GTT	TTG	ACC	GCT	ATT	TTC	637
118	Leu	Asp	Pro	Ile	Phe	Ala	Val	Leu	Ser	Asp	Val	Leu	Thr	Ala	Ile	Phe	
119						160					165			170			
121	CAG	GAT	ACC	GTA	CGT	GCA	GAA	ATG	ACC	AAA	GTA	TTG	GCA	CCA	GCA	TTC	685
122	Gln	Asp	Thr	Val	Arg	Ala	Glu	Met	Thr	Lys	Val	Leu	Ala	Pro	Ala	Phe	
123						175					180			185			
125	AAA	AAA	GAA	TTG	GAA	CGA	AAC	AAC	CAA	TAGACTTACA	CACAAACATAAA						732
126	Lys	Lys	Glu	Leu	Glu	Arg	Asn	Asn	Gln								
127	190					195											
129	CACTGTTATT	TTTACACTGG	ATAATCAAAT	GAAATAAATT	TTTTTATCAT	TTTGTTAAA											792

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Input Set : N:\Crf3\RULE60\10024955.raw
 Output Set: N:\CRF3\04162002\J024955.raw

131 AAAAAAAAAA AAAAAAAA 812
 134 (2) INFORMATION FOR SEQ ID NO: 2:
 136 (i) SEQUENCE CHARACTERISTICS:
 137 (A) LENGTH: 215 amino acids
 138 (B) TYPE: amino acid
 139 (D) TOPOLOGY: linear
 141 (ii) MOLECULE TYPE: protein
 143 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 145 Met Met Leu Leu Leu Ile Ala Ala Ala Ala Phe Val Ala Val Ser
 146 -17 -15 -10 -5
 148 Ala Asp Pro Ile His Tyr Asp Lys Ile Thr Glu Glu Ile Asn Lys Ala
 149 1 5 10 15
 151 Val Asp Glu Ala Val Ala Ala Ile Glu Lys Ser Glu Thr Phe Asp Pro
 152 20 25 30
 154 Met Lys Val Pro Asp His Ser Asp Lys Phe Glu Arg His Ile Gly Ile
 155 35 40 45
 157 Ile Asp Leu Lys Gly Glu Leu Asp Met Arg Asn Ile Gln Val Arg Gly
 158 50 55 60
 160 Leu Lys Gln Met Lys Arg Val Gly Asp Ala Asn Val Lys Ser Glu Asp
 161 65 70 75
 163 Gly Val Val Lys Ala His Leu Leu Val Gly Val His Asp Asp Val Val
 164 80 85 90 95
 166 Ser Met Glu Tyr Asp Leu Ala Tyr Lys Leu Gly Asp Leu His Pro Asn
 167 100 105 110
 169 Thr His Val Ile Ser Asp Ile Gln Asp Phe Val Val Glu Leu Ser Leu
 170 115 120 125
 172 Glu Val Ser Glu Glu Gly Asn Met Thr Leu Thr Ser Phe Glu Val Arg
 173 130 135 140
 175 Gln Phe Ala Asn Val Val Asn His Ile Gly Gly Leu Ser Ile Leu Asp
 176 145 150 155
 178 Pro Ile Phe Ala Val Leu Ser Asp Val Leu Thr Ala Ile Phe Gln Asp
 179 160 165 170 175
 181 Thr Val Arg Ala Glu Met Thr Lys Val Leu Ala Pro Ala Phe Lys Lys
 182 180 185 190
 184 Glu Leu Glu Arg Asn Asn Gln
 185 195
 187 (2) INFORMATION FOR SEQ ID NO: 3:
 189 (i) SEQUENCE CHARACTERISTICS:
 190 (A) LENGTH: 18 base pairs
 191 (B) TYPE: nucleic acid
 192 (C) STRANDEDNESS: single
 193 (D) TOPOLOGY: linear
 195 (ii) MOLECULE TYPE: cDNA
 199 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 201 GATCCAATTG ACTATGAT 18
 203 (2) INFORMATION FOR SEQ ID NO: 4:
 205 (i) SEQUENCE CHARACTERISTICS:
 206 (A) LENGTH: 17 base pairs
 207 (B) TYPE: nucleic acid

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Output Set: N:\CRF3\04162002\J024955.raw

208 (C) STRANDEDNESS: single
 209 (D) TOPOLOGY: linear
 211 (ii) MOLECULE TYPE: cDNA
 215 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 217 GGTGAATTAG ACATGCG
 219 (2) INFORMATION FOR SEQ ID NO: 5:
 221 (i) SEQUENCE CHARACTERISTICS:
 222 (A) LENGTH: 24 base pairs
 223 (B) TYPE: nucleic acid
 224 (C) STRANDEDNESS: single
 225 (D) TOPOLOGY: linear
 227 (ii) MOLECULE TYPE: cDNA
 231 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 233 TCAATTTGG ATCCAATTT CGCT
 235 (2) INFORMATION FOR SEQ ID NO: 6:
 237 (i) SEQUENCE CHARACTERISTICS:
 238 (A) LENGTH: 761 base pairs
 239 (B) TYPE: nucleic acid
 240 (C) STRANDEDNESS: single
 241 (D) TOPOLOGY: linear
 243 (ii) MOLECULE TYPE: cDNA
 246 (ix) FEATURE:
 247 (A) NAME/KEY: CDS
 248 (B) LOCATION: 43..681
 251 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 253 GATCTTATAT CAATAACAAT CCAAAAAAAC ATATCTTACA AA ATG ATG AAA TTT Met Met Lys Phe
 254 5 10 15 20
 255 1
 257 TTG TTG ATT GCT GCC GTG GCA TTT GTC GCC GTT TCG GCT GAT CCA ATT 102
 258 Leu Leu Ile Ala Ala Val Ala Phe Val Ala Val Ser Ala Asp Pro Ile
 259 5 10 15 20
 261 CAC TAT GAT AAA ATC ACC GAA GAA ATC AAC AAA GCT ATT GAT GAT GCC 150
 262 His Tyr Asp Lys Ile Thr Glu Glu Ile Asn Lys Ala Ile Asp Asp Ala
 263 25 30 35
 265 ATT GCT GCT ATT GAA CAA TCC GAA ACA ATA GAT CCA ATG AAA GTA CCT 198
 266 Ile Ala Ala Ile Glu Gln Ser Glu Thr Ile Asp Pro Met Lys Val Pro
 267 40 45 50
 269 GAT CAT GCC GAT AAA TTC GAA CGT CAT GTT GGT ATT GTG GAT TTC AAA 246
 270 Asp His Ala Asp Lys Phe Glu Arg His Val Gly Ile Val Asp Phe Lys
 271 55 60 65
 273 GGT GAA TTA GCC ATG CGA AAC ATT GAG GCT CGA GGA TTG AAA CAA ATG 294
 274 Gly Glu Leu Ala Met Arg Asn Ile Glu Ala Arg Gly Leu Lys Gln Met
 275 70 75 80
 277 AAA CGT CAA GGT GAT GCT AAT GTC AAA GGT GAA GAG GGT ATT GTT AAA 342
 278 Lys Arg Gln Gly Asp Ala Asn Val Lys Gly Glu Glu Gly Ile Val Lys
 279 85 90 95 100
 281 GCT CAT TTG TTG ATC GGT GTT CAC GAT GAT ATC GTC TCG ATG GAA TAT 390
 282 Ala His Leu Leu Ile Gly Val His Asp Asp Ile Val Ser Met Glu Tyr
 283 105 110 115

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285	GAT	TTA	GCA	TAC	AAA	TTG	GGT	GAT	CTT	CAT	CCA	ACC	ACT	CAT	GTC	ATT		438
286	Asp	Leu	Ala	Tyr	Lys	Leu	Gly	Asp	Leu	His	Pro	Thr	Thr	His	Val	Ile		
287				120					125					130				
289	TCG	GAT	ATT	CAA	GAT	TTT	GTT	GCC	TTG	TCC	CTT	GAA	ATT	TCT	GAT		486	
290	Ser	Asp	Ile	Gln	Asp	Phe	Val	Val	Ala	Leu	Ser	Leu	Glu	Ile	Ser	Asp		
291				135					140				145					
293	GAA	GGT	AAC	ATA	ACA	ATG	ACA	TCT	TTT	GAA	GTA	CGA	CAA	TTC	GCT	AAT		534
294	Glu	Gly	Asn	Ile	Thr	Met	Thr	Ser	Phe	Glu	Val	Arg	Gln	Phe	Ala	Asn		
295				150					155			160						
297	GTT	GTC	AAC	CAT	ATT	GGT	GGT	CTT	TCA	ATC	TTG	GAT	CCA	ATT	TTT	GGC		582
298	Val	Val	Asn	His	Ile	Gly	Gly	Leu	Ser	Ile	Leu	Asp	Pro	Ile	Phe	Gly		
299				165					170			175		180				
301	GTT	TTA	TCT	GAT	GTA	TTG	ACC	GCT	ATT	TTC	CAA	GAC	ACC	GTA	CGT	AAG		630
302	Val	Leu	Ser	Asp	Val	Leu	Thr	Ala	Ile	Phe	Gln	Asp	Thr	Val	Arg	Lys		
303				185					190			195						
305	GAA	ATG	ACC	AAA	GTA	TTG	GCA	CCA	GCA	TTT	AAA	CGT	GAA	TTG	GAA	AAA		678
306	Glu	Met	Thr	Lys	Val	Leu	Ala	Pro	Ala	Phe	Lys	Arg	Glu	Leu	Glu	Lys		
307				200					205			210						
309	AAT	TAACCAATAG	ACATCATT	TTT	TCCA	ACTG	TA	CAAT	CT	CT	AT	TTC	ACTG	A	C	A		731
310	Asn																	
313	ATAAAATAAA	ATTTTAT	TTT	TTATTTCTCC														761
316	(2)	INFORMATION FOR SEQ ID NO: 7:																
318	(i)	SEQUENCE CHARACTERISTICS:																
319	(A)	LENGTH: 213 amino acids																
320	(B)	TYPE: amino acid																
321	(D)	TOPOLOGY: linear																
323	(ii)	MOLECULE TYPE: protein																
325	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 7:																
327	Met	Met	Lys	Phe	Leu	Leu	Ile	Ala	Ala	Val	Ala	Phe	Val	Ala	Val	Ser		
328	1				5				10					15				
330	Ala	Asp	Pro	Ile	His	Tyr	Asp	Lys	Ile	Thr	Glu	Glu	Ile	Asn	Lys	Ala		
331					20				25				30					
333	Ile	Asp	Asp	Ala	Ile	Ala	Ala	Ile	Glu	Gln	Ser	Glu	Thr	Ile	Asp	Pro		
334					35				40				45					
336	Met	Lys	Val	Pro	Asp	His	Ala	Asp	Lys	Phe	Glu	Arg	His	Val	Gly	Ile		
337					50				55			60						
339	Val	Asp	Phe	Lys	Gly	Glu	Leu	Ala	Met	Arg	Asn	Ile	Glu	Ala	Arg	Gly		
340					65				70			75		80				
342	Leu	Lys	Gln	Met	Lys	Arg	Gln	Gly	Asp	Ala	Asn	Val	Lys	Gly	Glu	Glu		
343						85				90			95					
345	Gly	Ile	Val	Lys	Ala	His	Leu	Leu	Ile	Gly	Val	His	Asp	Asp	Ile	Val		
346					100				105			110						
348	Ser	Met	Glu	Tyr	Asp	Leu	Ala	Tyr	Lys	Leu	Gly	Asp	Leu	His	Pro	Thr		
349					115				120			125						
351	Thr	His	Val	Ile	Ser	Asp	Ile	Gln	Asp	Phe	Val	Val	Ala	Leu	Ser	Leu		
352					130				135			140						
354	Glu	Ile	Ser	Asp	Glu	Gly	Asn	Ile	Thr	Met	Thr	Ser	Phe	Glu	Val	Arg		
355					145				150			155		160				
357	Gln	Phe	Ala	Asn	Val	Val	Asn	His	Ile	Gly	Gly	Leu	Ser	Ile	Leu	Asp		

VERIFICATION SUMMARY

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L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]